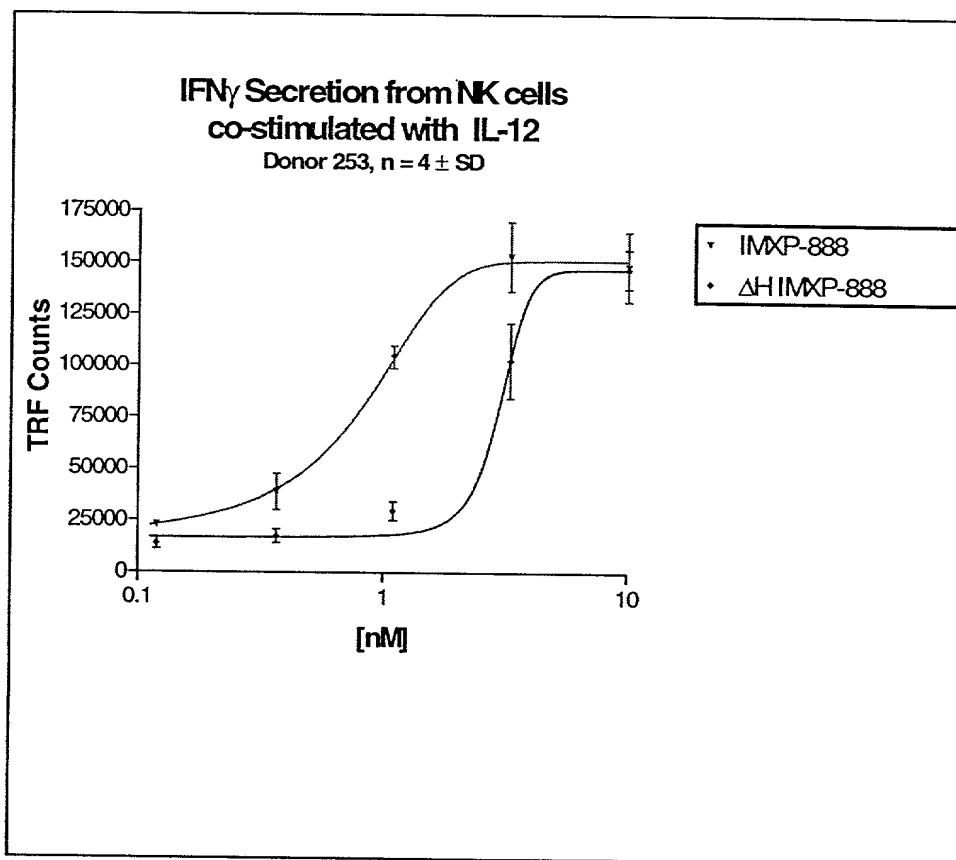


FIGURE 1



mumlsa3935c7.pep x mumlsa3935c2.pep (Murine splice variants)

1 MTRSPALLLLLLGALPSAEAARGPPRMADKVVPRQVARLGRTVRLQCPVE 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MTRSPALLLLLLGALPSAEAAR..... 22

101 FGSLSVNYTLIIMDDISPGKESPGPGGSSGGQEDPASQQWARPRFTQPSK 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
23 DDISPGKESPGPGGSSGGQEDPASQQWARPRFTQPSK 59

151 MRRRVIARPVGSSVRLKCVASGHPRPDIMWMKDDQTLTHLEASEHRKKW 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
60 MRRRVIARPVGSSVRLKCVASGHPRPDIMWMKDDQTLTHLEASEHRKKW 109

201 TLSLKNLKPEDSGKYTCRVSNKAGAINATYKVDVIQRTRSKPVLTGTHPV 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
110 TLSLKNLKPEDSGKYTCRVSNKAGAINATYKVDVIQRTRSKPVLTGTHPV 159

251 NTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGSEGRNSTIDVGGQKFV 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
160 NTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGSEGRNSTIDVGGQKFV 209

301 VLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGYSFRSAFLT 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
210 VLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGYSFRSAFLT 259

351 VLPDPKPPGPPMASSSSSTSLPWPVIVIGIPAGAVFILGTVLLWLCQTKKK 400
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
260 VLPDPKPPGPPMASSSSSTSLPWPVIVIGIPAGAVFILGTVLLWLCQTKKK 309

401 PCAPASTLPVPGHRPPGTSRERSGDKDLPSSLAVGICEEHGSAMAPQHILA 450
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
310 PCAPASTLPVPGHRPPGTSRERSGDKDLPSSLAVGICEEHGSAMAPQHILA 359

451 SGSTAGPKLYPKLYTDVHTHTHTCTHTLSCGGQGSSTPACPLSVLNTA 500
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
360 SGSTAGPKLYPKLYTDVHTHTHTCTHTLSCGGQGSSTPACPLSVLNTA 409

501 NLQALCPEVGIWGPQQVGRRIENNNGRVS 529
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
410 NLQALCPEVGIWGPQQVGRRIENNNGRVS 438

FIGURE 2

Mouse:	1	MTRSPALLLLL-----LGALP SAE AARG PPRMADKVVPRQ VARL GRTVRL QCP VEGD P PPL	56
Human:	1	MTPSPLL LPLL PPLL GAFF PAAA ARGP PKMADKVVPRQ VARL GRTVRL QCP VEGD P PPL	60
Mouse:	57	TMWTKD GRTI THSGW SRF RVL PQGL KVKE VEAE DAGV YVCK ATNG F GSL SVN YT LIMDDI	116
Human:	61	TMWTKD GRTI THSGW SRF RVL PQGL KVKV QVER E DAGV YVCK ATNG F GSL SVN YT LUV LD DI	120
Mouse:	117	SPG KES PPG GSS GG QED PAS Q QWARP RFT QPS KMRR RVIA RP VGS SVRL KCVA SGH PRP	176
Human:	121	SPG KES LGP DSS SGG QED PAS Q QWARP RFT QPS KMRR RVIA RP VGS SVRL KCVA SGH PRP	180
Mouse:	177	DIM MMK DQ TLTH LEASE H RKKW T LSL KNL K PED SG KYTC RVSN KAGA INAT YKV DV IQ	236
Human:	181	DIT W M K DQ ALTR PEA E PRKKW T LSL KNL R PED SG KYTC RVSN RA GAINAT YKV DV IQ	240
Mouse:	237	RTR SKP VL TG TH PVNT TVDF GGT TSF QCK VRS DV KPV I QWL KR VEY GSE GRH NSTD VGG	296
Human:	241	RTR SKP VL TG TH PVNT TVDF GGT TSF QCK VRS DV KPV I QWL KR VEY GAE GRH NSTD VGG	300
Mouse:	297	QKF VVL PT GDV WSR RD GS YLN KLL ISR ARQ DD AGM YIC LGA NT MG YSF RSA FLTV LPDPK	356
Human:	301	QKF VVL PT GDV WSR RD GS YLN KLL IT RARQ DD AGM YIC LGA NT MG YSF RSA FLTV LPDPK	360
Mouse:	357	PPG PMA SSS SSTS L PWP VVIG IPAG AV FIL GT YLL WL CQT KKK PCAP AST L PVP GHR PRP	416
Human:	361	PPG PVA SSS SAT S L PWP VVIG IPAG AV FIL GT YLL WL CQA QKK PCAP APP L PGP HRP	420
Mouse:	417	GTS RER SGD KDL PSL A-----VGI CEE EHGSAMA QPH ILAS GSTA GPK LYK LYTD VH T	469
Human:	421	GTARD RSG DKDL PSL AALS AG PG VGL CEE HGSP AA PHILL GP GP VAG PK LYK LYTD VH T	480
Mouse:	470	HHT HTCT H LSC GQGS ST PACPL SVL INTA NLQ ALC PE VGI WG PRQQ VGR IEN NG GRVS	529
Human:	481	HHT HTSH THS HT SHVE GKV H QHI HY QC 504 (SEQ ID NO: 3)	(SEQ ID NO: 1)

FIGURE 3